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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: Wed Jun 13 09:50:02 EDT 2007

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Application No: 10590661

Version No: 1.1

Input Set:

Output Set:

Started: 2007-06-13 09:49:55.205

Finished: 2007-06-13 09:49:55.802

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 597 ms

Total Warnings: 7

Total Errors: 0

No. of SeqIDs Defined: 11

Actual SeqID Count: 11

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)

# SEQUENCE LISTING

<110> HAYASHI, HIROAKI  
INOUE, KENICHIRO  
HOSHINO, MASATERU  
SHIBUYA, MASAAKI  
EBIZUKA, YUTAKA

<120> TRITERPENE HYDROXYLASE

<130> Q96763

<140> 10/590,661

<141> 2006-08-25

<150> PCT/JP05/03205

<151> 2005-02-25

<150> JP 2004-049123

<151> 2004-02-25

<160> 11

<170> PatentIn version 3.3

<210> 1

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
primer

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gactcgagtc gacaacgatt tttttttttt tt

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aaacactagt atgctagaca tcaaaggcta c

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<210> 6

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<223> Description of Artificial Sequence: Synthetic primer

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taaggctagc ctaaagatct tgatgagttg c

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<212> DNA

<213> Soybean

<220>

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1                  5                  10                  15	

tca acc att ctg ata cgt tcc atc ttc aag aaa cca cag cgt cta aga	96
Ser Thr Ile Leu Ile Arg Ser Ile Phe Lys Lys Pro Gln Arg Leu Arg	
20                  25                  30	

ctc cca ccg ggt cct cca att tca gta ccc ttg ctg gga cac gcg cca	144
Leu Pro Pro Gly Pro Pro Ile Ser Val Pro Leu Leu Gly His Ala Pro	
35                  40                  45	

tat ctc cgt tca ctg ctc cac caa gcc ttg tac aag cta tca ctg cgc	192
Tyr Leu Arg Ser Leu Leu His Gln Ala Leu Tyr Lys Leu Ser Leu Arg	
50                  55                  60	

tat gga ccc ttg atc cac gtc atg atc ggt tgc aag cac gtg gtg gtg	240
Tyr Gly Pro Leu Ile His Val Met Ile Gly Ser Lys His Val Val Val	
65                  70                  75                  80	

gcg tgc tgc gcg gag acg gcc aag cag atc ctc aaa acc tgc gag gag	288
Ala Ser Ser Ala Glu Thr Ala Lys Gln Ile Leu Lys Thr Ser Glu Glu	
85                  90                  95	

gca ttc tgc aac cgt ccc tta atg ata gcg agc gag agc cta acc tac	336
Ala Phe Cys Asn Arg Pro Leu Met Ile Ala Ser Glu Ser Leu Thr Tyr	
100                  105                  110	

ggc gcg gcg gac tac ttc ttc atc ccc tac ggc aca tac tgg cgg ttc	384
Gly Ala Ala Asp Tyr Phe Phe Ile Pro Tyr Gly Thr Tyr Trp Arg Phe	
115                  120                  125	

ctg aag aag ctc tgc atg acg gag ctt ctg agc ggg aag acc ctg gag	432
Leu Lys Lys Leu Cys Met Thr Glu Leu Leu Ser Gly Lys Thr Leu Glu	
130                  135                  140	

cat ttc gtg aga atc cgc gag agc gag gtg gag gcg ttc ctc aag aga	480
His Phe Val Arg Ile Arg Glu Ser Glu Val Glu Ala Phe Leu Lys Arg	
145                  150                  155                  160	

atg atg gag att tca ggc aat gga aat tac gag gtg gtg atg agg aag	528
Met Met Glu Ile Ser Gly Asn Gly Asn Tyr Glu Val Val Met Arg Lys	
165                  170                  175	

gag ctc ata acg cac acg aat aac atc atc acg agg atg ata atg ggg	576
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Glu Leu Ile Thr His Thr Asn Asn Ile Ile Thr Arg Met Ile Met Gly	
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aag aag agt aat gcg gaa aac gat gag gtg gcc agg ttg agg aag gtg	624
Lys Lys Ser Asn Ala Glu Asn Asp Glu Val Ala Arg Leu Arg Lys Val	
195 200 205	
gtg agg gag gtc ggg gag ttg ctt ggg gcg ttt aac ttg ggg gat gtt	672
Val Arg Glu Val Gly Glu Leu Leu Gly Ala Phe Asn Leu Gly Asp Val	
210 215 220	
att ggg ttc atg agg cct ttg gat ctg caa ggg ttt ggg aag aag aac	720
Ile Gly Phe Met Arg Pro Leu Asp Leu Gln Gly Phe Gly Lys Lys Asn	
225 230 235 240	
atg gaa act cac cac aag gtg gat gcg atg atg gag aag gtg ttg agg	768
Met Glu Thr His His Lys Val Asp Ala Met Met Glu Lys Val Leu Arg	
245 250 255	
gag cat gag gag gct agg gct aag gaa gat gct gac tct gat agg aag	816
Glu His Glu Glu Ala Arg Ala Lys Glu Asp Ala Asp Ser Asp Arg Lys	
260 265 270	
aag gat ctt ttt gat att ttg ttg aac ctc att gaa gct gat ggt gct	864
Lys Asp Leu Phe Asp Ile Leu Leu Asn Leu Ile Glu Ala Asp Gly Ala	
275 280 285	
gac aat aag ctc act aga gag agt gcc aaa gcc ttt gct ctg gac atg	912
Asp Asn Lys Leu Thr Arg Glu Ser Ala Lys Ala Phe Ala Leu Asp Met	
290 295 300	
ttc atc gcc ggc aca aac ggc ccc gca agc gtc cta gag tgg tca ctg	960
Phe Ile Ala Gly Thr Asn Gly Pro Ala Ser Val Leu Glu Trp Ser Leu	
305 310 315 320	
gcg gag ctg gtg aga aac ccc cac gtt ttc aag aag gca aga gaa gag	1008
Ala Glu Leu Val Arg Asn Pro His Val Phe Lys Lys Ala Arg Glu Glu	
325 330 335	
att gag tca gtg gta ggc aaa gaa agg ctg gtc aaa gaa tca gac att	1056
Ile Glu Ser Val Val Gly Lys Glu Arg Leu Val Lys Glu Ser Asp Ile	
340 345 350	
ccc aac cta cca tac cta caa gca ttg ctg aag gaa acc cta agg ctg	1104
Pro Asn Leu Pro Tyr Leu Gln Ala Leu Leu Lys Glu Thr Leu Arg Leu	
355 360 365	
cac ccg cca acc cca ata ttc gca aga gaa gcc atg cga aca tgc cag	1152
His Pro Pro Thr Pro Ile Phe Ala Arg Glu Ala Met Arg Thr Cys Gln	
370 375 380	
gtt gaa ggc tac gac att ccg gaa aat tcc act att ttg atc agc aca	1200
Val Glu Gly Tyr Asp Ile Pro Glu Asn Ser Thr Ile Leu Ile Ser Thr	
385 390 395 400	
tgg gcc att ggt agg gat cca aat tac tgg gat gac gca ctc gag tac	1248
Trp Ala Ile Gly Arg Asp Pro Asn Tyr Trp Asp Asp Ala Leu Glu Tyr	

405	410	415	
aag ccg gag agg ttc ttg ttc tcc	gac gac ccg ggc aag agc aag att	1296	
Lys Pro Glu Arg Phe Leu Phe Ser	Asp Asp Pro Gly Lys Ser Lys Ile		
420	425 430		
gac gtg agg ggg cag tac tat cag	ctc ctg ccc ttt ggg agc ggg aga	1344	
Asp Val Arg Gly Gln Tyr Tyr Gln	Leu Leu Pro Phe Gly Ser Gly Arg		
435	440 445		
aga agc tgc ccc gga gcc tcg cta	gcg ttg ctt gtc atg caa gca acg	1392	
Arg Ser Cys Pro Gly Ala Ser Leu	Ala Leu Leu Val Met Gln Ala Thr		
450	455 460		
cta gcg agt ttg atc cag tgc ttc	gac tgg atc gtt aat gat ggt aaa	1440	
Leu Ala Ser Leu Ile Gln Cys Phe	Asp Trp Ile Val Asn Asp Gly Lys		
465	470 475 480		
aac cat cat gtt gac atg tct gag	gaa ggg agg gtg act gtg ttt ttg	1488	
Asn His His Val Asp Met Ser Glu	Glu Gly Arg Val Thr Val Phe Leu		
485	490 495		
gcc aag cca ctc aag tgc aag cct	gtt ccg cgt ttc act ccg ttc gct	1536	
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gcc tga		1542	
Ala			

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Ser Thr Ile Leu Ile Arg Ser Ile Phe Lys Lys Pro Gln Arg Leu Arg  
 20 25 30

Leu Pro Pro Gly Pro Pro Ile Ser Val Pro Leu Leu Gly His Ala Pro  
 35 40 45

Tyr Leu Arg Ser Leu Leu His Gln Ala Leu Tyr Lys Leu Ser Leu Arg  
 50 55 60

Tyr Gly Pro Leu Ile His Val Met Ile Gly Ser Lys His Val Val Val  
 65 70 75 80

Ala Ser Ser Ala Glu Thr Ala Lys Gln Ile Leu Lys Thr Ser Glu Glu  
85 90 95

Ala Phe Cys Asn Arg Pro Leu Met Ile Ala Ser Glu Ser Leu Thr Tyr  
100 105 110

Gly Ala Ala Asp Tyr Phe Phe Ile Pro Tyr Gly Thr Tyr Trp Arg Phe  
115 120 125

Leu Lys Lys Leu Cys Met Thr Glu Leu Leu Ser Gly Lys Thr Leu Glu  
130 135 140

His Phe Val Arg Ile Arg Glu Ser Glu Val Glu Ala Phe Leu Lys Arg  
145 150 155 160

Met Met Glu Ile Ser Gly Asn Gly Asn Tyr Glu Val Val Met Arg Lys  
165 170 175

Glu Leu Ile Thr His Thr Asn Asn Ile Ile Thr Arg Met Ile Met Gly  
180 185 190

Lys Lys Ser Asn Ala Glu Asn Asp Glu Val Ala Arg Leu Arg Lys Val  
195 200 205

Val Arg Glu Val Gly Glu Leu Leu Gly Ala Phe Asn Leu Gly Asp Val  
210 215 220

Ile Gly Phe Met Arg Pro Leu Asp Leu Gln Gly Phe Gly Lys Lys Asn  
225 230 235 240

Met Glu Thr His His Lys Val Asp Ala Met Met Glu Lys Val Leu Arg  
245 250 255

Glu His Glu Glu Ala Arg Ala Lys Glu Asp Ala Asp Ser Asp Arg Lys  
260 265 270

Lys Asp Leu Phe Asp Ile Leu Leu Asn Leu Ile Glu Ala Asp Gly Ala  
275 280 285

Asp Asn Lys Leu Thr Arg Glu Ser Ala Lys Ala Phe Ala Leu Asp Met  
290 300

Phe Ile Ala Gly Thr Asn Gly Pro Ala Ser Val Leu Glu Trp Ser Leu



305 310 315 320

Ala Glu Leu Val Arg Asn Pro His Val Phe Lys Lys Ala Arg Glu Glu  
325 330 335

Ile Glu Ser Val Val Gly Lys Glu Arg Leu Val Lys Glu Ser Asp Ile  
340 345 350

Pro Asn Leu Pro Tyr Leu Gln Ala Leu Leu Lys Glu Thr Leu Arg Leu  
355 360 365

His Pro Pro Thr Pro Ile Phe Ala Arg Glu Ala Met Arg Thr Cys Gln  
370 375 380

Val Glu Gly Tyr Asp Ile Pro Glu Asn Ser Thr Ile Leu Ile Ser Thr  
385 390 395 400

Trp Ala Ile Gly Arg Asp Pro Asn Tyr Trp Asp Asp Ala Leu Glu Tyr  
405 410 415

Lys Pro Glu Arg Phe Leu Phe Ser Asp Asp Pro Gly Lys Ser Lys Ile  
420 425 430

Asp Val Arg Gly Gln Tyr Tyr Gln Leu Leu Pro Phe Gly Ser Gly Arg  
435 440 445

Arg Ser Cys Pro Gly Ala Ser Leu Ala Leu Leu Val Met Gln Ala Thr  
450 455 460

Leu Ala Ser Leu Ile Gln Cys Phe Asp Trp Ile Val Asn Asp Gly Lys  
465 470 475 480

Asn His His Val Asp Met Ser Glu Glu Gly Arg Val Thr Val Phe Leu  
485 490 495

Ala Lys Pro Leu Lys Cys Lys Pro Val Pro Arg Phe Thr Pro Phe Ala  
500 505 510

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<210> 10

<211> 1542

<212> DNA

<213> Soybean

<220>

<221> CDS

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Met Leu Asp Ile Lys Gly Tyr Leu Val Leu Phe Phe Leu Trp Phe Ile	
1 5 10 15	

tca acc att ctg ata cgt tcc atc ttc aag aaa cca cag cgt cta aga	96
Ser Thr Ile Leu Ile Arg Ser Ile Phe Lys Lys Pro Gln Arg Leu Arg	
20 25 30	

ctc cca ccg ggt cct cca att tca ata ccc ttg ctg gga cac gcg cca	144
Leu Pro Pro Gly Pro Pro Ile Ser Ile Pro Leu Leu Gly His Ala Pro	
35 40 45	

tat ctc cgt tca ctg ctc cac caa gca ttg tac aag cta tca ctg cgc	192
Tyr Leu Arg Ser Leu Leu His Gln Ala Leu Tyr Lys Leu Ser Leu Arg	
50 55 60	

tat gga ccc ttg atc cac gtc atg atc ggt tcg aag cac gtg gtg gtg	240
Tyr Gly Pro Leu Ile His Val Met Ile Gly Ser Lys His Val Val Val	
65 70 75 80	

gcg tcg tcg gcg gag acg gcc aag cag atc ctc aaa acc tcg gag gag	288
Ala Ser Ser Ala Glu Thr Ala Lys Gln Ile Leu Lys Thr Ser Glu Glu	
85 90 95	

gca ttc tgc aac cgt ccc tta atg ata gcg agc gag agc cta acc tac	336
Ala Phe Cys Asn Arg Pro Leu Met Ile Ala Ser Glu Ser Leu Thr Tyr	
100 105 110	

ggc gcg gcg gac tac ttc ttc atc ccc tac ggc aca tac tgg cgg ttc	384
Gly Ala Ala Asp Tyr Phe Phe Ile Pro Tyr Gly Thr Tyr Trp Arg Phe	
115 120 125	

ctg aag aag ctc tgc atg acg gag ctt ctg agc ggg aag acc ctg gag	432
Leu Lys Lys Leu Cys Met Thr Glu Leu Leu Ser Gly Lys Thr Leu Glu	
130 135 140	

cat ttc gtg aga atc cgc gag agc gag gtg gag gcg ttc ctc aag aga	480
His Phe Val Arg Ile Arg Glu Ser Glu Val Glu Ala Phe Leu Lys Arg	
145 150 155 160	

atg atg gag att tca ggc aat gga aat tac gag gtg gtg atg agg aag	528
Met Met Glu Ile Ser Gly Asn Gly Asn Tyr Glu Val Val Met Arg Lys	
165 170 175	

gag ctc ata acg cac acg aat aac atc atc acg agg atg ata atg ggg	576
Glu Leu Ile Thr His Thr Asn Asn Ile Ile Thr Arg Met Ile Met Gly	
180 185 190	

aag aag agt aat gcg gaa aac gat gag gtg gcc agg ttg agg aag gtg	624
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Lys Lys Ser Asn Ala Glu Asn Asp Glu Val Ala Arg Leu Arg Lys Val  
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Val Arg Glu Val Gly Glu Leu Leu Gly Ala Phe Asn Leu Gly Asp Val  
210 215 220

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Ile Gly Phe Met Arg Pro Leu Asp Leu Gln Gly Phe Gly Lys Lys Asn  
225 230 235 240

atg gaa act cac cac aag gtg gat gcg atg atg gag aag gtg ttg agg 768  
Met Glu Thr His His Lys Val Asp Ala Met Met Glu Lys Val Leu Arg  
245 250 255

gag cat gag gag gct agg gct aag gaa gat gct gac tct gat agg aag 816  
Glu His Glu Glu Ala Arg Ala Lys Glu Asp Ala Asp Ser Asp Arg Lys  
260 265 270

aag gat ctt ttt gat